

**IN THE CLAIMS:**

1-28. (cancelled).

29. (new) A composition comprising a circular vector, wherein said circular vector comprises:

- a) a toxic gene sequence,
- b) a nucleic acid sequence, wherein said nucleic acid sequence comprises;
  - i) first and second ends,
  - ii) a selectable marker region,
  - iii) an origin of replication, and
  - iv) a first transcriptional terminator downstream of said selectable marker region;
- c) a second transcriptional terminator between said toxic gene sequence and said first end; and
- d) a third transcriptional terminator between said toxic gene sequence and said second end.

30. (new) The composition of Claim 29, wherein said first transcriptional terminator is configured to terminate RNA transcripts encoded by at least one selectable marker sequence in said selectable marker region.

31. (new) The composition of Claim 29, wherein said nucleic acid sequence further comprises a first non-promoter sequence between said first end and said selectable marker region, and a second non-promoter sequence between said second end and said selectable marker region, wherein each of said first and second non-promoter sequences are unable to serve as an operable promoter in a host cell.

32. (new) The composition of Claim 29, wherein said selectable marker region comprises first and second selectable marker sequences.

33. (new) The composition of Claim 29, wherein said circular vector further comprises two primer binding sites.

34. (new) The composition of Claim 29, wherein said toxic gene, when expressed, is configured to prevent growth of a host cell.

35. (new) A method of forming a vector component comprising;

a) providing;

i) a composition comprising a first circular vector, wherein said first circular vector comprises:

A) a toxic gene sequence,

B) a nucleic acid sequence, wherein said nucleic acid sequence comprises;

I) first and second ends,

II) a selectable marker region,

III) an origin of replication, and

IV) a first transcriptional terminator downstream of said selectable marker region;

C) a second transcriptional terminator between said toxic gene sequence and said first end;

D) a third transcriptional terminator between said toxic gene sequence and said second end;

E) a first restriction enzyme recognition site between said toxic gene sequence and said second transcriptional terminator; and

F) a second restriction enzyme recognition site between said toxic gene sequence and said third transcriptional terminator; and

ii) one or more restriction enzymes; and

b) mixing said composition with said one or more restriction enzymes such that said first circular vector is cleaved at said first and second restriction enzyme recognition sites, thereby generating a vector component with first and second free ends.

36. (new) The method of Claim 35, wherein said first transcriptional terminator is configured to terminate RNA transcripts encoded by at least one selectable marker sequence in said selectable marker region.

37. (new) The method of Claim 35, wherein said nucleic acid sequence comprises a first non-promoter sequence between said first end and said selectable marker region, and a second non-promoter sequence between said second end and said selectable marker region, wherein each of said first and second non-promoter sequences are unable to serve as an operable promoter in a host cell.

38. (new) The method of Claim 35, wherein said selectable marker region comprises first and second selectable marker sequences.

39. (new) The method of Claim 35, wherein said first circular vector further comprises two primer binding sites.

40. (new) The method of Claim 35, wherein said toxic gene, when expressed, is configured to prevent growth of a host cell.

41. (new) The method of Claim 35, further comprising step c) mixing said vector component with a library of insert sequences under condition such that a second circular vector is generated, wherein said second circular vector comprises at least one insert sequence.